RAW SEQUENCE LISTING

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Application Serial Number: _10/617,443 C_
Source: _1F4/6_
Date Processed by STIC: _5/1/06_

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RAW SEQUENCE LISTING   DATE: 05/02/2006
PATENT APPLICATION: **US/10/617,443C**   TIME: 08:54:28

Input Set : **N:\Crf4\05012006\J617443D.raw**
Output Set: **N:\CRF4\05012006\J617443C.raw**

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 1 <110> APPLICANT: DARROW, ANDREW LAWRENCE
 2        QI, JIAN-SHEN
 3        CHEN, CAILIN
 4        ANDRADE-GORDON, PATRICIA
 5 <120> TITLE OF INVENTION: HUMAN PRSS11-LIKE S2 SERINE PROTEASE AND USES THEREOF
 6 <130> FILE REFERENCE: ORT-1644-CIP
C-->  7 <140> CURRENT APPLICATION NUMBER: US/10/617,443C
 8 <141> CURRENT FILING DATE: 2003-07-02
 9 <150> PRIOR APPLICATION NUMBER: 10/189,099
10 <151> PRIOR FILING DATE: 2002-07-03
11 <160> NUMBER OF SEQ ID NOS: 31
12 <170> SOFTWARE: PatentIn Ver. 3.3
14 <210> SEQ ID NO: 1
15 <211> LENGTH: 3006
16 <212> TYPE: DNA
17 <213> ORGANISM: Homo sapiens
18 <400> SEQUENCE: 1
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21       ggccacacag ctagaaagca gccaggccca gccgaacccc tggtgtgtgc agcccccagc 180
22       ccagttgctc attgcggggc tcgggagcca cgagcgaggc tgagcagcat gtgttccaga 240
23       tggtgggaac tggagagagc ccggcacagg cccgtgcagg aaccccgag ggctgtaggc 300
24       cccgtgccac tgcatgcctc aggcctgtgg tcctggcagc cacagccct actgctgacg 360
25       gcagcaggaa tctgagcccg ggaagggtcc agggaagttc gtgaaccatc tagcaagtcg 420
26       ggctggggtg tggccaagtt agacacagat gtagggccct gtggactcag aaattggcag 480
27       ctcttttggc ccagagggggc cacgctgtgt ccgggcctgg gtagctcaga agggtcacct 540
28       gggggtcttc cactacaccc ccgcctggac actgctgtag ccccagggct cggagggacc 600
29       agctggagcc catgaggaga gggccagttc tctcctgtaa gggtattgct gtagcatgag 660
30       ggaacagaca aggcccaggg ggactaaccc gagatccagc cccggcctca ctcccgtgtg 720
31       gctcacggca atatcctaac ctctctctga gcctcctgcc cagcctagca gggtccagtg 780
32       agggggggtga ggaagcccag cacgtggaag ccttttttaac cattctcggg gtgagcgagc 840
33       cccttcccaa atgcctggtg tcactgcact gctgtgtggt aggggggtccc caacgggctc 900
34       agtgtgggct gaggctggct ctgaactggg acagggtct caggaagagc ctcctcctcc 960
35       tgcccactgg gcataggcct ctgggagctg gcagcatcgt gatctcactg atgcacctgg 1020
36       cccttcccgc cagcgcaggt ctccaccagc tgagcagccc gcgctacaag ttcaacttca 1080
37       ttgctgacgt ggtggagaag atcgcaccag ccgtggtcca catagagctc ttcctgagac 1140
38       acccgctgtt tggccgcaac gtgccctgt ccagcggttc tggcttcatc atgtcagagg 1200
39       ccggcctgat catcaccaat gcccacgtgg tgtccagcaa cagtgctgcc ccgggcaggc 1260
40       agcagctcaa ggtgcagcta cagaatgggg actcctatga ggccaccatc aaagacatcg 1320
41       acaagaagtc ggacattgcc accatcaaga tccatcccaa gaaaaagctc cctgtgttgt 1380
42       tgctgggtca ctcggccgac ctgcggcctg gggagtttgt ggtggccatc ggcagtccct 1440
43       tcgccctaca gaacacagtg acaacgggca tcgtcagcac tgcccagcgg gagggcaggg 1500
44       agctgggcct ccgggactcc gacatggact acatccagac ggatgccatc atcaactacg 1560
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45      ggaactccgg gggaccactg gtgaacctgg atggcgaggt cattggcatc aacacgctca 1620
46      aggtcacggc tggcatctcc tttgccatcc cctcagaccg catcacacgg ttcctcacag 1680
47      agttccaaga caagcagatc aaagactgga agaagcgctt catcggcata cggatgcgga 1740
48      cgatcacacc aagcctggtg gatgagctga aggccagcaa cccggacttc ccagaggtca 1800
49      gcagtggaat ttatgtgcaa gaggttgcgc cgaattcacc ttctcagaga ggcggcatcc 1860
50      aagatggtga catcatcgtc aaggtcaacg ggcgtcctct agtggactcg agtgagctgc 1920
51      aggaggccgt gctgaccgag tctcctctcc tactggaggt gcggcggcgg aacgacgacc 1980
52      tcctcttcag catcgcacct gaggtggtca tgtgaggggc gcattcctcc agcgccaagc 2040
53      gtcagagcct gcagacaacg gagggcagcg cccccccgag atcaggacga aggaccaccg 2100
54      tcggtcctca gcagggcggc agcctcctcc tggctgtccg gggcagagcg gaggctgggc 2160
55      ttggccaggg gcccgaattt ccgcctgggg agtgttggat ccacatcccg gtgccgggga 2220
56      gggaagccca acatcccctt gtacagatga tcctgaaagt cacttccaag ttctccggat 2280
57      attcacaaaa ctgccttcca tggaggtccc ctcctctcct agcttcccgc ctctgcccct 2340
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59      aagcttcttc cccctgaca aacgcccacc tgacctgagg ccccagcttc cctctgccct 2460
60      aggacttacc aagctgtagg gccagggctg ctgcctgcca gcctggggtc cctggaggac 2520
61      aggtcacatc tgatcccttt ggggtgcggg ggtggggtcc agcccagagc aggcactgag 2580
62      tgaatgcccc ctggctgcgg agctgagccc cgccctgcca tgaggttttc ctccccaggc 2640
63      aggcaggagg ccgcggggag cacgtggaaa gttggctgct gcctggggaa gcttctcctc 2700
64      cccaaggcgg ccatggggca gcctgcagag acagtggac gtggagctgc ggggtgtgag 2760
65      gactgagccg gcttcccctt cccacgcagc tctgggatgc agcagccgct cgcatggaag 2820
66      tgccgcccag aggcatgcag gctgctgggc accacccccct catccaggga acgagtgtgt 2880
67      ctcaaggggc atttgtgagc tttgctgtaa atggattccc agtgttgctt gtactgtatg 2940
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69      aaaaaa                                                           3006
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71 <210> SEQ ID NO: 2
72 <211> LENGTH: 334
73 <212> TYPE: PRT
74 <213> ORGANISM: Homo sapiens
75 <400> SEQUENCE: 2

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76      Met His Leu Ala Leu Pro Ala Ser Ala Gly Leu His Gln Leu Ser Ser
77       1               5                  10                  15
78      Pro Arg Tyr Lys Phe Asn Phe Ile Ala Asp Val Val Glu Lys Ile Ala
79                  20                  25                  30
80      Pro Ala Val Val His Ile Glu Leu Phe Leu Arg His Pro Leu Phe Gly
81                  35                  40                  45
82      Arg Asn Val Pro Leu Ser Ser Gly Ser Gly Phe Ile Met Ser Glu Ala
83          50                  55                  60
84      Gly Leu Ile Ile Thr Asn Ala His Val Val Ser Ser Asn Ser Ala Ala
85          65                  70                  75                  80
86      Pro Gly Arg Gln Gln Leu Lys Val Gln Leu Gln Asn Gly Asp Ser Tyr
87                      85                  90                  95
88      Glu Ala Thr Ile Lys Asp Ile Asp Lys Lys Ser Asp Ile Ala Thr Ile
89                  100                 105                 110
90      Lys Ile His Pro Lys Lys Lys Leu Pro Val Leu Leu Leu Gly His Ser
91              115                 120                 125
92      Ala Asp Leu Arg Pro Gly Glu Phe Val Val Ala Ile Gly Ser Pro Phe
93          130                 135                 140
94      Ala Leu Gln Asn Thr Val Thr Thr Gly Ile Val Ser Thr Ala Gln Arg
```

```
95       145                 150                 155                 160
96       Glu Gly Arg Glu Leu Gly Leu Arg Asp Ser Asp Met Asp Tyr Ile Gln
97                       165                 170                 175
98       Thr Asp Ala Ile Ile Asn Tyr Gly Asn Ser Gly Gly Pro Leu Val Asn
99                   180                 185                 190
100      Leu Asp Gly Glu Val Ile Gly Ile Asn Thr Leu Lys Val Thr Ala Gly
101              195             200             205
102      Ile Ser Phe Ala Ile Pro Ser Asp Arg Ile Thr Arg Phe Leu Thr Glu
103          210                 215                 220
104      Phe Gln Asp Lys Gln Ile Lys Asp Trp Lys Lys Arg Phe Ile Gly Ile
105      225                 230                 235                 240
106      Arg Met Arg Thr Ile Thr Pro Ser Leu Val Asp Glu Leu Lys Ala Ser
107                      245                 250                 255
108      Asn Pro Asp Phe Pro Glu Val Ser Ser Gly Ile Tyr Val Gln Glu Val
109                  260                 265                 270
110      Ala Pro Asn Ser Pro Ser Gln Arg Gly Gly Ile Gln Asp Gly Asp Ile
111              275                 280                 285
112      Ile Val Lys Val Asn Gly Arg Pro Leu Val Asp Ser Ser Glu Leu Gln
113          290                 295                 300
114      Glu Ala Val Leu Thr Glu Ser Pro Leu Leu Leu Glu Val Arg Arg Gly
115      305                 310                 315                 320
116      Asn Asp Asp Leu Leu Phe Ser Ile Ala Pro Glu Val Val Met
117                      325                 330
119 <210> SEQ ID NO: 3
120 <211> LENGTH: 23
121 <212> TYPE: DNA
122 <213> ORGANISM: Artificial Sequence
123 <220> FEATURE:
124 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
125       primer
126 <400> SEQUENCE: 3
127       cagccgtgac cttgagcgtg ttg                                      23
129 <210> SEQ ID NO: 4
130 <211> LENGTH: 22
131 <212> TYPE: DNA
132 <213> ORGANISM: Artificial Sequence
133 <220> FEATURE:
134 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
135       primer
136 <400> SEQUENCE: 4
137       ggccgagtga cccagcaaca ac                                       22
139 <210> SEQ ID NO: 5
140 <211> LENGTH: 34
141 <212> TYPE: DNA
142 <213> ORGANISM: Artificial Sequence
143 <220> FEATURE:
144 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
145       primer
146 <400> SEQUENCE: 5
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147        cgtgtctaga gccatgcacc tggcccttcc cgcc                      34
149 <210> SEQ ID NO: 6
150 <211> LENGTH: 30
151 <212> TYPE: DNA
152 <213> ORGANISM: Artificial Sequence
153 <220> FEATURE:
154 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
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157        gcgctctaga catgaccacc tcaggtgcga                           30
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161 <212> TYPE: DNA
162 <213> ORGANISM: Artificial Sequence
163 <220> FEATURE:
164 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
165        primer
166 <400> SEQUENCE: 7
167        gcaagtcggg ctggggtgtg                                      20
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170 <211> LENGTH: 24
171 <212> TYPE: DNA
172 <213> ORGANISM: Artificial Sequence
173 <220> FEATURE:
174 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
175        primer
176 <400> SEQUENCE: 8
177        cagggagctt tttcttggga tgga                                 24
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180 <211> LENGTH: 480
181 <212> TYPE: PRT
182 <213> ORGANISM: Homo sapiens
183 <400> SEQUENCE: 9
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186        Ala Ala Pro Ala Ser Ala Gln Leu Ser Arg Ala Gly Arg Ser Ala Pro
187                       20                  25                  30
188        Leu Ala Ala Gly Cys Pro Asp Arg Cys Glu Pro Ala Arg Cys Pro Pro
189                   35                  40                  45
190        Gln Pro Glu His Cys Glu Gly Gly Arg Ala Arg Asp Ala Cys Gly Cys
191             50                  55                  60
192        Cys Glu Val Cys Gly Ala Pro Glu Gly Ala Ala Cys Gly Leu Gln Glu
193          65                  70                  75                  80
194        Gly Pro Cys Gly Glu Gly Leu Gln Cys Val Val Pro Phe Gly Val Pro
195                           85                  90                  95
196        Ala Ser Ala Thr Val Arg Arg Arg Ala Gln Ala Gly Leu Cys Val Cys
197                       100                 105                 110
198        Ala Ser Ser Glu Pro Val Cys Gly Ser Asp Ala Asn Thr Tyr Ala Asn
199                   115                 120                 125
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200        Leu Cys Gln Leu Arg Ala Ala Ser Arg Arg Ser Glu Arg Leu His Arg
201            130                 135                 140
202        Pro Pro Val Ile Val Leu Gln Arg Gly Ala Cys Gly Gln Gly Gln Glu
203        145                 150                 155                 160
204        Asp Pro Asn Ser Leu Arg His Lys Tyr Asn Phe Ile Ala Asp Val Val
205                        165                 170                 175
206        Glu Lys Ile Ala Pro Ala Val Val His Ile Glu Leu Phe Arg Lys Leu
207                        180                 185                 190
208        Pro Phe Ser Lys Arg Glu Val Pro Val Ala Ser Gly Ser Gly Phe Ile
209                        195                 200                 205
210        Val Ser Glu Asp Gly Leu Ile Val Thr Asn Ala His Val Val Thr Asn
211            210                 215                 220
212        Lys His Arg Val Lys Val Glu Leu Lys Asn Gly Ala Thr Tyr Glu Ala
213        225                 230                 235                 240
214        Lys Ile Lys Asp Val Asp Glu Lys Ala Asp Ile Ala Leu Ile Lys Ile
215                        245                 250                 255
216        Asp His Gln Gly Lys Leu Pro Val Leu Leu Leu Gly Arg Ser Ser Glu
217                        260                 265                 270
218        Leu Arg Pro Gly Glu Phe Val Val Ala Ile Gly Ser Pro Phe Ser Leu
219            275                 280                 285
220        Gln Asn Thr Val Thr Thr Gly Ile Val Ser Thr Thr Gln Arg Gly Gly
221            290                 295                 300
222        Lys Glu Leu Gly Leu Arg Asn Ser Asp Met Asp Tyr Ile Gln Thr Asp
223        305                 310                 315                 320
224        Ala Ile Ile Asn Tyr Gly Asn Ser Gly Gly Pro Leu Val Asn Leu Asp
225                        325                 330                 335
226        Gly Glu Val Ile Gly Ile Asn Thr Leu Lys Val Thr Ala Gly Ile Ser
227                        340                 345                 350
228        Phe Ala Ile Pro Ser Asp Lys Ile Lys Lys Phe Leu Thr Glu Ser His
229                        355                 360                 365
230        Asp Arg Gln Ala Lys Gly Lys Ala Ile Thr Lys Lys Lys Tyr Ile Gly
231            370                 375                 380
232        Ile Arg Met Met Ser Leu Thr Ser Ser Lys Ala Lys Glu Leu Lys Asp
233        385                 390                 395                 400
234        Arg His Arg Asp Phe Pro Asp Val Ile Ser Gly Ala Tyr Ile Ile Glu
235                        405                 410                 415
236        Val Ile Pro Asp Thr Pro Ala Glu Ala Gly Gly Leu Lys Glu Asn Asp
237                        420                 425                 430
238        Val Ile Ile Ser Ile Asn Gly Gln Ser Val Val Ser Ala Asn Asp Val
239            435                 440                 445
240        Ser Asp Val Ile Lys Arg Glu Ser Thr Leu Asn Met Val Val Arg Arg
241            450                 455                 460
242        Gly Asn Glu Asp Ile Met Ile Thr Val Ile Pro Glu Glu Ile Asp Pro
243        465                 470                 475                 480
245  <210> SEQ ID NO: 10
246  <211> LENGTH: 458
247  <212> TYPE: PRT
248  <213> ORGANISM: Homo sapiens
249  <400> SEQUENCE: 10
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VERIFICATION SUMMARY   DATE: 05/02/2006
PATENT APPLICATION: **US/10/617,443C**   TIME: 08:54:29

Input Set : **N:\Crf4\05012006\J617443D.raw**
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L:7 M:270 C: Current Application Number differs, Wrong Format